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RAW SEQUENCE LISTING

DATE: 09/23/2002

PATENT APPLICATION: US/09/823,394

TIME: 10:20:32

Input Set : A:\SALKINS.012CP1.TXT

Output Set: N:\CRF3\09232002\I823394.raw

4 <110> APPLICANT: Chory, Joanne
 5 Jianming, Li
 6 Salk Institute for Biological Studies
 8 <120> TITLE OF INVENTION: RECEPTOR KINASE, BIN 1
 11 <130> FILE REFERENCE: SALKINS.012CP1
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/823,394
 C--> 13 <141> CURRENT FILING DATE: 2001-03-30
 13 <150> PRIOR APPLICATION NUMBER: 08/881,706
 14 <151> PRIOR FILING DATE: 1997-06-24
 16 <160> NUMBER OF SEQ ID NOS: 2
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 4104
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Arabidopsis
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (97)...(3684)
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 31 cttccacac ttttctctct cacaaaactct tgagaa atg aag act ttt tca agc 114
 32 Met Lys Thr Phe Ser Ser
 33 1 5
 35 ttc ttt ctc tct gta aca act ctc ttc ttc ttc tcc ttc ttt tct ctt 162
 36 Phe Phe Leu Ser Val Thr Thr Leu Phe Phe Phe Ser Phe Phe Ser Leu
 37 10 15 20
 39 tca ttt caa gct tca cca tct cag tct tta tac aga gaa atc cat cag 210
 40 Ser Phe Gln Ala Ser Pro Ser Gln Ser Leu Tyr Arg Glu Ile His Gln
 41 25 30 35
 43 ctt ata agc ttc aaa gac gtt ctt cct gac aag aat ctt ctc cca gac 258
 44 Leu Ile Ser Phe Lys Asp Val Leu Pro Asp Lys Asn Leu Leu Pro Asp
 45 40 45 50
 47 tgg tct tcc aac aaa aac ccg tgt act ttc gat ggc gtt act tgc aga 306
 48 Trp Ser Ser Asn Lys Asn Pro Cys Thr Phe Asp Gly Val Thr Cys Arg
 49 55 60 65 70
 51 gac gac aaa gtt act tcg att gat ctc agc tcc aag cct ctc aac gtc 354
 52 Asp Asp Lys Val Thr Ser Ile Asp Leu Ser Ser Lys Pro Leu Asn Val
 53 75 80 85
 55 gga ttc agt gcc gtg tcc tcg tct ctc ctg tct ctc acc gga tta gag 402
 56 Gly Phe Ser Ala Val Ser Ser Ser Leu Leu Ser Leu Thr Gly Leu Glu
 57 90 95 100
 59 tct ctg ttt ctc tca aac tca cac atc aat ggc tcc gtt tct ggc ttc 450
 60 Ser Leu Phe Leu Ser Asn Ser His Ile Asn Gly Ser Val Ser Gly Phe

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63 aag tgc tct gct tct tta acc agc ttg gat cta tct aga aac tct ctt	498			
64 Lys Cys Ser Ala Ser Leu Thr Ser Leu Asp Leu Ser Arg Asn Ser Leu				
65 120 125 130				
67 tcg ggt cct gta acg act cta aca agc ctt ggt tct tgc tcc ggt ctg	546			
68 Ser Gly Pro Val Thr Thr Leu Thr Ser Leu Gly Ser Cys Ser Gly Leu				
69 135 140 145 150				
71 aag ttt ctt aac gtc tct tcc aat aca ctt gat ttt ccc ggg aaa gtt	594			
72 Lys Phe Leu Asn Val Ser Ser Asn Thr Leu Asp Phe Pro Gly Lys Val				
73 155 160 165				
75 tca ggt ggg ttg aag cta aac agc ttg gaa gtt ctg gat ctt tct gcg	642			
76 Ser Gly Gly Leu Lys Leu Asn Ser Leu Glu Val Leu Asp Leu Ser Ala				
77 170 175 180				
79 aat tca atc tcc ggt gct aac gtc gtt ggt tgg gtt ctc tcc gat ggg	690			
80 Asn Ser Ile Ser Gly Ala Asn Val Val Gly Trp Val Leu Ser Asp Gly				
81 185 190 195				
83 tgt gga gag ttg aaa cat tta gcg att agc gga aac aaa atc agt gga	738			
84 Cys Gly Glu Leu Lys His Leu Ala Ile Ser Gly Asn Lys Ile Ser Gly				
85 200 205 210				
87 gac gtc gat gtt tct cgc tgc gtg aat ctc gag ttt ctc gat gtt tcc	786			
88 Asp Val Asp Val Ser Arg Cys Val Asn Leu Glu Phe Leu Asp Val Ser				
89 215 220 225 230				
91 tcc aac aat ttc tcc act ggg att cct ttc ctc gga gat tgc tct gct	834			
92 Ser Asn Asn Phe Ser Thr Gly Ile Pro Phe Leu Gly Asp Cys Ser Ala				
93 235 240 245				
95 ctg caa cat ctt gac atc tcc ggg aac aaa tta tcc ggc gat ttc tcc	882			
96 Leu Gln His Leu Asp Ile Ser Gly Asn Lys Leu Ser Gly Asp Phe Ser				
97 250 255 260				
99 cgt gct atc tct act tgc aca gag ctc aag ttg ttg aac atc tct agt	930			
100 Arg Ala Ile Ser Thr Cys Thr Glu Leu Lys Leu Leu Asn Ile Ser Ser				
101 265 270 275				
103 aac caa ttc gtc gga cca atc cct ccg cta ccg ctt aaa agt ctc caa	978			
104 Asn Gln Phe Val Gly Pro Ile Pro Pro Leu Pro Leu Lys Ser Leu Gln				
105 280 285 290				
107 tac ctc tct ctg gcc gag aac aaa ttc acc ggc gag atc cct gac ttt	1026			
108 Tyr Leu Ser Leu Ala Glu Asn Lys Phe Thr Gly Glu Ile Pro Asp Phe				
109 295 300 305 310				
111 ctc tcc ggc gcg tgt gat aca ctc act ggt ctc gat ctc tct gga aat	1074			
112 Leu Ser Gly Ala Cys Asp Thr Leu Thr Gly Leu Asp Leu Ser Gly Asn				
113 315 320 325				
115 cat ttc tac ggt gcg gtt cct cca ttc ttc ggt tca tgt tct ctt ctc	1122			
116 His Phe Tyr Gly Ala Val Pro Pro Phe Phe Gly Ser Cys Ser Leu Leu				
117 330 335 340				
119 gaa tca ctc gcg ttg tcg agt aac aac ttc tct ggc gag tta ccg atg	1170			
120 Glu Ser Leu Ala Leu Ser Ser Asn Phe Ser Gly Glu Leu Pro Met				
121 345 350 355				
123 gat acg ttg ttg aag atg aga gga ctc aaa gta ctt gat ctg tct ttc	1218			
124 Asp Thr Leu Leu Lys Met Arg Gly Leu Lys Val Leu Asp Leu Ser Phe				
125 360 365 370				

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127 aac gag ttt tcc ggc gaa tta ccg gaa tct ctg acg aat cta tcc gct 1266
128 Asn Glu Phe Ser Gly Glu Leu Pro Glu Ser Leu Thr Asn Leu Ser Ala
129 375 380 385 390
131 tcg ttg cta acg tta gat ctc agc tcc aac aat ttc tcc ggt ccg att 1314
132 Ser Leu Leu Thr Leu Asp Leu Ser Ser Asn Asn Phe Ser Gly Pro Ile
133 395 400 405
135 ctc cca aat ctc tgc cag aac cct aaa aac act ctg cag gag ctt tac 1362
136 Leu Pro Asn Leu Cys Gln Asn Pro Lys Asn Thr Leu Gln Glu Leu Tyr
137 410 415 420
139 ctt cag aac aat ggc ttc acc ggg aag att cca ccg act tta agc aac 1410
140 Leu Gln Asn Asn Gly Phe Thr Gly Lys Ile Pro Pro Thr Leu Ser Asn
141 425 430 435
143 tgt tct gag ctg gtt tcg ctt cac ttg agc ttc aat tac ctc tcc ggg 1458
144 Cys Ser Glu Leu Val Ser Leu His Leu Ser Phe Asn Tyr Leu Ser Gly
145 440 445 450
147 aca atc cct tcg agc tta ggc tct cta tcg aag ctt cga gat ctg aaa 1506
148 Thr Ile Pro Ser Ser Leu Gly Ser Leu Ser Lys Leu Arg Asp Leu Lys
149 455 460 465 470
151 cta tgg ctg aat atg tta gaa gga gag atc cct cag gag ctc atg tat 1554
152 Leu Trp Leu Asn Met Leu Glu Gly Glu Ile Pro Gln Glu Leu Met Tyr
153 475 480 485
155 gtc aag acc tta gag act ctg atc ctc gac ttc aac gat tta acc ggt 1602
156 Val Lys Thr Leu Glu Thr Leu Ile Leu Asp Phe Asn Asp Leu Thr Gly
157 490 495 500
159 gaa atc cct tcc ggt tta agt aac tgt acc aat ctt aac tgg att tct 1650
160 Glu Ile Pro Ser Gly Leu Ser Asn Cys Thr Asn Leu Asn Trp Ile Ser
161 505 510 515
163 ctg tcg aat aac cgg tta acc ggt gag att ccg aaa tgg att ggc cgg 1698
164 Leu Ser Asn Asn Arg Leu Thr Gly Glu Ile Pro Lys Trp Ile Gly Arg
165 520 525 530
167 tta gag aat ctc gct atc ctc aag tta agc aac aat tca ttc tcc ggg 1746
168 Leu Glu Asn Leu Ala Ile Leu Lys Leu Ser Asn Asn Ser Phe Ser Gly
169 535 540 545 550
171 aac att ccg gat gag ctc ggc gac tgc aga agc tta atc tgg ctt gat 1794
172 Asn Ile Pro Asp Glu Leu Gly Asp Cys Arg Ser Leu Ile Trp Leu Asp
173 555 560 565
175 ctc aac acc aat ctc ttc aat gga acg att ccg gcg gcg atg ttt aaa 1842
176 Leu Asn Thr Asn Leu Phe Asn Gly Thr Ile Pro Ala Ala Met Phe Lys
177 570 575 580
179 caa tcc ggg aaa atc gct gcc aat ttc atc gcc ggt aag agg tac gtt 1890
180 Gln Ser Gly Lys Ile Ala Ala Asn Phe Ile Ala Gly Lys Arg Tyr Val
181 585 590 595
183 tat atc aaa aac gat ggg atg aag aaa gag tgt cat gga gct ggt aat 1938
184 Tyr Ile Lys Asn Asp Gly Met Lys Lys Glu Cys His Gly Ala Gly Asn
185 600 605 610
187 tta ctt gag ttt caa gga atc aga tcc gaa caa tta aac cgg ctt tca 1986
188 Leu Leu Glu Phe Gln Gly Ile Arg Ser Glu Gln Leu Asn Arg Leu Ser
189 615 620 625 630
191 acg agg aac cct tgt aat atc act agc aga gtc tat gga ggt cac act 2034

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192	Thr	Arg	Asn	Pro	Cys	Asn	Ile	Thr	Ser	Arg	Val	Tyr	Gly	Gly	His	Thr	
193					635					640					645		
195	tcg	ccg	acg	ttt	gat	aac	aat	ggt	tcg	atg	atg	ttt	ctg	gac	atg	tct	2082
196	Ser	Pro	Thr	Phe	Asp	Asn	Asn	Gly	Ser	Met	Met	Phe	Leu	Asp	Met	Ser	
197				650					655					660			
199	tac	aac	atg	ttg	tct	gga	tac	ata	ccg	aag	gag	att	ggt	tcg	atg	cct	2130
200	Tyr	Asn	Met	Leu	Ser	Gly	Tyr	Ile	Pro	Lys	Glu	Ile	Gly	Ser	Met	Pro	
201			665					670					675				
203	tat	ctg	ttt	att	ctc	aat	ttg	ggt	cat	aac	gat	atc	tct	ggt	tcg	att	2178
204	Tyr	Leu	Phe	Ile	Leu	Asn	Leu	Gly	His	Asn	Asp	Ile	Ser	Gly	Ser	Ile	
205		680					685					690					
207	cct	gat	gag	gta	ggt	gat	cta	aga	ggt	tta	aac	att	ctt	gat	ctt	tca	2226
208	Pro	Asp	Glu	Val	Gly	Asp	Leu	Arg	Gly	Leu	Asn	Ile	Leu	Asp	Leu	Ser	
209	695					700				705						710	
211	agc	aat	aag	ctc	gat	ggg	agg	att	ccg	cag	gct	atg	tca	gct	ctt	act	2274
212	Ser	Asn	Lys	Leu	Asp	Gly	Arg	Ile	Pro	Gln	Ala	Met	Ser	Ala	Leu	Thr	
213				715					720					725			
215	atg	ctt	acg	gaa	atc	gat	ttg	tcg	aat	aat	aat	ttg	tct	ggt	ccg	att	2322
216	Met	Leu	Thr	Glu	Ile	Asp	Leu	Ser	Asn	Asn	Asn	Leu	Ser	Gly	Pro	Ile	
217			730					735					740				
219	cct	gag	atg	ggt	cag	ttt	gag	act	ttt	cca	ccg	gct	aag	ttc	ttg	aac	2370
220	Pro	Glu	Met	Gly	Gln	Phe	Glu	Thr	Phe	Pro	Pro	Ala	Lys	Phe	Leu	Asn	
221			745					750					755				
223	aat	cct	ggt	ctc	tgt	ggt	tat	cct	ctt	ccg	cgg	tgt	gat	cct	tca	aat	2418
224	Asn	Pro	Gly	Leu	Cys	Gly	Tyr	Pro	Leu	Pro	Arg	Cys	Asp	Pro	Ser	Asn	
225		760				765						770					
227	gca	gac	ggt	tat	gct	cat	cat	cag	aga	tct	cat	gga	agg	aga	cca	gcg	2466
228	Ala	Asp	Gly	Tyr	Ala	His	His	Gln	Arg	Ser	His	Gly	Arg	Arg	Pro	Ala	
229	775				780				785						790		
231	tcc	ctt	gct	ggt	agt	gtg	gcg	atg	gga	ttg	ttg	ttc	tct	ttt	gtg	tgt	2514
232	Ser	Leu	Ala	Gly	Ser	Val	Ala	Met	Gly	Leu	Leu	Phe	Ser	Phe	Val	Cys	
233				795					800					805			
235	ata	ttt	ggg	ctg	atc	ctt	gtt	ggt	aga	gag	atg	agg	aag	aga	cgg	aga	2562
236	Ile	Phe	Gly	Leu	Ile	Leu	Val	Gly	Arg	Glu	Met	Arg	Lys	Arg	Arg	Arg	
237			810					815					820				
239	aag	aaa	gag	gcg	gag	ttg	gag	atg	tat	gcg	gaa	gga	cat	gga	aac	tct	2610
240	Lys	Lys	Glu	Ala	Glu	Leu	Glu	Met	Tyr	Ala	Glu	Gly	His	Gly	Asn	Ser	
241			825					830					835				
243	ggc	gat	aga	act	gct	aac	aac	acc	aat	tgg	aag	ctg	act	ggt	gtg	aaa	2658
244	Gly	Asp	Arg	Thr	Ala	Asn	Asn	Thr	Asn	Trp	Lys	Leu	Thr	Gly	Val	Lys	
245		840				845						850					
247	gaa	gcc	ttg	agt	atc	aat	ctt	gct	gct	ttc	gag	aag	cca	ttg	cgg	aag	2706
248	Glu	Ala	Leu	Ser	Ile	Asn	Leu	Ala	Ala	Phe	Glu	Lys	Pro	Leu	Arg	Lys	
249	855				860				865					870			
251	ctc	acg	ttt	gcg	gat	ctt	ctt	cag	gct	acc	aat	ggt	ttc	cat	aat	gat	2754
252	Leu	Thr	Phe	Ala	Asp	Leu	Leu	Gln	Ala	Thr	Asn	Gly	Phe	His	Asn	Asp	
253				875					880					885			
255	agt	ctg	att	ggt	tct	ggt	ggg	ttt	gga	gat	gtt	tac	aaa	gcg	att	ttg	2802
256	Ser	Leu	Ile	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Val	Tyr	Lys	Ala	Ile	Leu	

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263	caa	ggt	gat	aga	gag	ttc	atg	gcg
264	Gln	Gly	Asp	Arg	Glu	Phe	Met	Ala
265		920		925		930		
267	aaa	cat	cga	aat	ctt	gtg	cct	ctt
268	Lys	His	Arg	Asn	Leu	Val	Pro	Leu
269	935			940		945		950
271	gag	cgg	ctt	ctt	gtt	aat	gag	gtt
272	Glu	Arg	Leu	Leu	Val	Asn	Glu	Val
273				955		960		965
275	gtt	ttg	caa	gac	ccc	aag	aaa	ggt
276	Val	Leu	Gln	Asp	Pro	Lys	Lys	Gly
277				970		975		980
279	cgg	cgg	aag	att	gcg	ata	gga	tca
280	Arg	Arg	Lys	Ile	Ala	Ile	Gly	Ser
281				985		990		995
283	cac	aac	tgc	agt	ccg	cat	atc	atc
284	His	Asn	Cys	Ser	Pro	His	Ile	Ile
285		1000			1005			1010
287	gtg	ttg	ctt	gat	gag	aat	ttg	gaa
288	Val	Leu	Leu	Asp	Glu	Asn	Leu	Glu
289	1015			1020		1025		1030
291	gcg	agg	ctg	atg	agt	gcg	atg	gat
292	Ala	Arg	Leu	Met	Ser	Ala	Met	Asp
293				1035		1040		1045
295	gct	ggt	aca	ccg	ggt	tac	gtt	cct
296	Ala	Gly	Thr	Pro	Gly	Tyr	Val	Pro
297				1050		1055		1060
299	tgt	tca	aca	aaa	gga	gac	gtt	tat
300	Cys	Ser	Thr	Lys	Gly	Asp	Val	Tyr
301				1065		1070		1075
303	cta	ctc	acg	ggt	aaa	cgg	cca	acg
304	Leu	Leu	Thr	Gly	Lys	Arg	Pro	Thr
305		1080			1085			1090
307	aac	ctt	ggt	gga	tgg	gtg	aaa	cag
308	Asn	Leu	Val	Gly	Trp	Val	Lys	Gln
309	1095			1100		1105		1110
311	gtg	ttt	gac	ccg	gag	ctt	atg	aag
312	Val	Phe	Asp	Pro	Glu	Leu	Met	Lys
313				1115		1120		1125
315	ctt	tta	caa	cat	tta	aaa	gtt	gcg
316	Leu	Leu	Gln	His	Leu	Lys	Val	Ala
317				1130		1135		1140
319	tgg	aga	cga	ccg	aca	atg	gta	caa
320	Trp	Arg	Arg	Pro	Thr	Met	Val	Gln
321				1145		1150		1155

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date